

Fig. 1

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165

Fig. 2

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu			
1	5	10	15
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His			
20	25	30	
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe			
35	40	45	
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp			
50	55	60	
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu			
65	70	75	80
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp			
85	90	95	
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu			
100	105	110	
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala			
115	120	125	
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val			
130	135	140	
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala			
145	150	155	160
Cys Arg Thr Gly Asp Arg			
165			

Fig. 3

GGAATTCAACCACCATGGGGGTGCACGAATGTCCCTGCCCTGGCTGTGGCTTCTCTGTCCT
1 -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGAACACCGAAGAGGGACAGGGA
M G V H E C P A W L W L L S L -

GCTGTCGCTCCCTCTGGGCCCTCCAGCTGGCGCCCCCCCCCGAATCGAGGGCCGCGC
61 -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCGGAGGGTCAGGACCCGCGGGGGGGCTTAGCTCCGGCGCG
L S L P L G L P V L G A P P R I T E G R A -

CCCACACGCCATCTGTGACAGCCGAGTCCCTGGAGAGGGTACCTTTGGAGGCCAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
GGGTGGTGGAGTAGACACTGTGGCTCAGGACCTCTCATGGAGAACCTCCGGTTCT
P P R L I C D S R V L E R Y L L E A K E -

GGCGAGAAATACGACGGGCTGTGCTGAACACTGCACTTGAAATGAGAAATACACTGT
181 -----+-----+-----+-----+-----+-----+ 240
CCGGCTTATAGTGTGCTCCGACACGACTTGACGTGCAACTTACTCTTATAGTGACA
A E N I T T G C A E H C S L N E N I T V -

CCCAAGACACCAAAGTTAATTCTATGCCCTGGAGAGGGATGGAGGTGGGCAAGGCCGT
241 -----+-----+-----+-----+-----+-----+ 300
GGGTCTGTGTTTCAATTAAAGATAACGACCTTCTCACCTCCAGCCGTGTCGGCA
P D T K V N F Y A W K R M E V G Q Q A V -

AGAAGTCGGCAGGGCTGGCCCTGCTGTGCGGAAGCTGTCTCGGGGCCAGGCCGT
301 -----+-----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCCGGACGGGACGACAGCCTCGACAGGACGCCGGTCCGGACAA
E V W Q G L A L L S E A V L R G Q A L L -

GGTCAACTCTTCCCAGCGTGGAGGCCCTGCACTGCACTGTGGATAAAGCCGTAGTGG
361 -----+-----+-----+-----+-----+-----+ 420
CCGTTGAGAAGGGTGGCACCTCGGGACGTCGACGTACACCTATTTCGGCAGTCACC
V N S S Q P W E P L Q L H V D K A V S G -

421 CCTTCGAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGGCCATCTCCCC
-----+-----+-----+-----+-----+-----+ 480
GGAAGCGTCGGAGTTGAGACGAAGCCCGAGACCTCGGGTCTTCCTCGGTAGAGGGG
L R S L T T L L R A L G A Q K E A I S P -

481 TCCAGATCGGGCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTCGCAA
-----+-----+-----+-----+-----+-----+ 540
AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCCTTGA
P D A A S A A P L R T I T A D T F R K L -

541 CTTCCGAGTCTACTCCAATTCTCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG
-----+-----+-----+-----+-----+-----+ 600
GAAGGCTCAGATGAGGTAAAGGAGGCCCTTTCGACTTCGACATGTGCCCCCTCCGGAC
F R V Y S N F L R G K L K L Y T G E A C -

601 CAGGACAGGGACAGATGACCAGGTGAC
-----+-----+----- 629
GTCCCTGCCCCGTCTACTGGTCCAGCTG
R T G D R * -

Fig. 4

GGAATTACCAACCATGGGGGTGCACGAATGCTCTGCCCTGGCTGTGGCTTCCTGTCCCT
1 -----+-----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGAACCGGAAGAGGGACAGGGA
M G V H E C P A W L W L L S L -

GCTGTCGCTCCCTCTGGGCCTCCCAGTCTCTGGGCoooooooooooooACACGCCCTCAT
61 -----+-----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGGGGGTGGTGGAGTA
L S L P L G L P V L G A P P A P P R L I -

CTGTGACAGCGAGCTGGAGAGGTACCTTGGAGGCCAAGGAGGCCAGAAATATCAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
GACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCTCCGGCTTTAGTG
C D S R V L E R Y L L E A K E A E N I T -

GACGGGCTGTGCTGAACACTGCAGCTGAATGAGAAATATCACTGTCCCAGACACCAAAGT
181 -----+-----+-----+-----+-----+-----+-----+ 240
CTGCCCGACACGACTTGTGACGTCGAACCTTACTTATACTGACAGGGCTGTGGTTCA
T G C A E H C S L N E N I T V P D T K V -

TAATTTCTATGCCCTGGAAGAGGATGGAGGTGGGGCAGCAGGCCGTAGAAGTCTGGCAGGG
241 -----+-----+-----+-----+-----+-----+-----+ 300
ATTAAGATACGGACCTCTCTACCTCCAGCCCGTGTCCGGCATCTCAGACCGTCCC
N F Y A W K R M E V G Q Q A V E V W Q G -

CTGGCCCTGCTGCGGAAGCTGCTCTGGGGGCAAGGCCCTGGTGGCAACTCTTCCA
301 -----+-----+-----+-----+-----+-----+-----+ 360
GGACCCGGACGACAGCCTTGCACAGGACGCCCGTCCGGACAACCGTGGAGAAGGT
L A L L S E A V L R G Q A L L V N S S Q -

GCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAAGCCGTCACTGGCTTCGAGCCTCAC
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGCACCCCTCGGGGACGTCGACGTACACCTTTCCGGCAGTCACCGGAAGCGTCGGAGTG
P W E P L Q L H V D K A V S G L R S L T -

CACTCTGCTTCGGGCTCTGGAGGCCAGAAGGAAGCCATCTCCCTCAGATGCCGCCTC
421 -----+-----+-----+-----+-----+ 480
GTGAGACGAAGCCCAGACCCCTCGGGCTTCTTCCTCGTAGAGGGGAGGTCTACGCCGGAG
T L L R A L G A Q K E A I S P P D A A S -

AGCTGCTCCACTCCGAACAATCACTGCTGACACTTCCGCAAACCTTCCGAGTCTACTC
481 -----+-----+-----+-----+-----+ 540
TCGACGAGGTGAGGGCTTGTAGTGACGACTGTGAAAGGCCTTGAGAAGGCTCAGATGAG
A A P L R T I T A D T F R K L F R V Y S -

CAATTCCCTCGGGAAAGCTGAAGCTGTACACAGGGAGGCCTGCAGGACAGGGACAG
541 -----+-----+-----+-----+-----+ 600
GTAAAGGAGGCCCTTCGACTTCGACATGTGTCCTCCGGACGTCCGTCCCCGTGTC
N F L R G K L K L Y T G E A C R T G D R -

ATGACCAGGTGAC
601 -----+--- 614
TACTGGTCCAGCTG
* -

Fig. 5

GGAATTCAACCACATGGGGGTGCACGAATGTCCTGCCCTGGCTGTGGCTTCTCCTGTCCCT
1 -----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGAACCGAAGAGGACAGGGA
M G V H E C P A W L W L L I S L -

GCTGTCGCTCCCCTGGGCTCCAGTCTGGCGCCCCCCCCGGCGCCCACTACGC
61 -----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCCGGGGGGGCGCGGGGTGATGCG
L S L P L G L P V L G A P P G A A H Y A -

CCACACGCTCATCTGTACAGCGAGTCTGGAGAGGTACCTCTGGAGGCAAGGA
121 -----+-----+-----+-----+-----+ 180
GGGTGGTGGAGTAGACACTGTCGCTCAGGACCTCTCATGGAAACCTCCGGTTCT
P P R L I C D S R V L E R Y L L E A K E -

GGCGGAGAATATCACGACGGCTGTGCTGAACACTGCAGCTGAATGAGAATATCAGT
181 -----+-----+-----+-----+-----+ 240
CCGGCTTATAGTGTGCGCACAGACTGTGACGCTGAACTACTCTTATAGTGACA
A E N I T T G C A E H C S L N E N I T V -

CCAGACACAAAGTTAATTCTATGCCTGGAAGAGGATGGAGGTGGGGCAGGCCGT
241 -----+-----+-----+-----+-----+ 300
GGGTCTGTGTTTCAATTAAAGATA CGGACCTCTCCACCTCCAGCCGTCGCCGCA
P D T K V N F Y A W K R M E V G Q Q A V -

AGAAGTCTGGCAGGGCTGGCCCTGCTGCTGGAAGCTGTCCTGCAGGCCGT
301 -----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCGGACCCGGACAGCACAGCTCGACAGGACGCCCGTCGGGACAA
E V W Q G L A L L S E A V L R G Q A L L -

GGTCAACTCTTCCCAGCCGTGGGAGCCCTGCAGCTGCATGTGGATAAAGCCGT
361 -----+-----+-----+-----+-----+ 420
CCAGTTGAGAAGGGTCCGGACCCCTCGGGACGTCGACGTCACCTATTTCGGCAGTCACC
V N S S Q P W E P L Q L H V D K A V S G -

CTTCGCAGCCTCACCACTCTGCTCGGGCTCTGGGAGCCCAGAACGGAGCCATCTCCCC
421 -----+-----+-----+-----+-----+-----+ 480
GGAAGCGTCGGAGTGTGAGACGAAGCCCAGACCCCTCGGGCTTCCTCGGTAGAGGGG
L R S L T T L L R A L G A Q K E A I S P -

TCCAGATGCGGCCTCAGCTGCTCACCGAACAACTACTGCTGACACTTCCGCAAAC
481 -----+-----+-----+-----+-----+-----+ 540
AGGTCTACGCCGGAGTCGACGAGGTGAGGGCTTGTAGTGACGACTGTGAAAGCGTTGA
P D A A S A A P L R T I T A D T F R K L -

CTTCGAGTCACTCCAATTCTCCGGGAAAGCTGAAGCTGTACACAGGGAGGCCTG
541 -----+-----+-----+-----+-----+-----+ 600
GAAGGCTCAGATGAGGTAAAGGAGGCCCTTCGACTTCGACATGTGTCCCCCTCGGAC
F R V Y S N F L R G K L K L Y T T G E A C -

CA~~G~~ACAGGGACAGATGACCAGGTGAC
601 -----+-----+-----+-----+ 629
GTCTGTCCCCGTCTACTGGTCCAGCTG
R T G D R * -